

IN THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

45. (Currently amended) An isolated nucleic Nucleie acid sequence, coding comprising for a both tapetum-specific and a pollen-specific promoter, wherein the nucleic acid sequence comprising comprises a range of at least 900 contiguous nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1.

46. (Currently amended) An isolated nucleic Nucleie acid sequence according to claim 45, wherein the nucleic acid sequence comprises a range of at least contiguous 1000 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1.

47. (Currently amended) An isolated nucleic Nucleie acid sequence according to claim 45, wherein the nucleic acid sequence comprises a range of at least 1500 contiguous nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1.

48. (Currently amended) An isolated nucleic Nucleie acid sequence according to claim 45, wherein the nucleic acid sequence comprises the sequence represented in SEQ.ID. No. 1.

49. (Currently amended) An isolated nucleic Nucleic acid sequence coding comprising for a both tapetum-specific and a pollen-specific promoter, wherein the nucleic acid sequence comprising comprises the sequence represented in SEQ.ID. No. 2.

50. (Withdrawn) Nucleic acid sequence coding for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising the sequence represented in SEQ.ID. No. 3.

51. (Currently amended) An expression Expression system, comprising at least one isolated nucleic acid coding comprising for a both tapetum-specific and a pollen-specific promoter, wherein the nucleic acid sequence comprising comprises a range of at least 900 contiguous nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1.

52. (Previously presented) The expression Expression system according to claim 51, further comprising at least one terminator and/or a linker.

53. (Currently amended) A nucleic Nucleic acid construct, comprising a nucleic acid sequence according to claim 45 and at least part of an expressible a nucleic acid sequence selected from the group comprising consisting of expressible nucleic acid sequences, which code for translation products, which have a direct or indirect action and functional nucleic acids.

54. (Currently amended) The nucleic Nucleic acid construct according to claim 53, wherein the said part of the expressible nucleic acid sequence or the complete expressible sequence is

connected in the sense direction with the nucleic acid sequence according to claims 45.

55. (Withdrawn) Nucleic acid sequence according to claim 53, wherein the expressible nucleic acid codes for an invertase.

56. (Withdrawn) Nucleic acid construct according to claim 55, characterized in that the part of the nucleic acid sequence of an invertase or the complete sequence of an invertase is connected in the antisense direction with the nucleic acid sequence according to claim 45.

57. (Withdrawn) Nucleic acid construct according to claim 55, characterized in that the invertase is of the type present in a structure selected from the group comprising anthers, tapetum, pollen precursor cells and pollen.

58. (Withdrawn) Nucleic acid construct according to claim 55, wherein the invertase comes from the organism or from the plant group including the species into which the nucleic acid construct is to be introduced.

59. (Withdrawn) Nucleic acid construct according to claim 55, wherein the organism is selected from the group comprising food plants, ornamental plants and medicinal plants.

60. (Currently amended) A vector comprising:

a nucleic acid sequence coding comprising for a both tapetum-specific and a pollen-specific promoter, wherein the nucleic acid sequence comprising comprises a range of at least

900 contiguous nucleotides upstream of the TATA box of the sequence ~~represented in~~ SEQ.ID. No. 1 and/or

an expression system comprising at least one of said nucleic acid sequences, and/or

a nucleic acid construct comprising at least one of said nucleic acid sequences and at least part of ~~an expressible a~~ nucleic acid sequence selected from the group ~~comprising~~ consisting of expressible nucleic acid sequences, which code for translation products, which have ~~a direct or indirect action and~~ functional nucleic acids.

61. (Currently amended) A cell comprising:

a isolated nucleic acid sequence ~~coding comprising for a~~ both tapetum-specific and a pollen-specific promoter, wherein the nucleic acid sequence ~~comprising~~ comprises a range of at least 900 contiguous nucleotides upstream of the TATA box of the sequence ~~represented in~~ SEQ.ID. No. 1 and/or

an expression system comprising at least one of said nucleic acid sequences, and/or

a nucleic acid construct comprising at least one of said nucleic acid sequences and at least part of ~~an expressible a~~ nucleic acid sequence selected from the group ~~comprising~~ consisting of expressible nucleic acid sequences, which code for translation products, which have ~~a direct or indirect action and~~ functional nucleic acids.

62. (Withdrawn) Cell, characterized in that the cell comprises a nucleic acid sequence according to claim 61, which is a promoter, and a nucleic acid coding for an inhibitor of an

intervase, the promoter controlling the expression of the inhibitor.

63. (Currently amended) The cell according to claim 61, wherein the cell is selected from the group comprising consisting of pollen cells, pollen precursor cells and tapetum cells.

64. (Previously presented) The cell according to claim 61, wherein the cell is an arrested a pollen cell arrested in the mononuclear microspore stage.

65. (Previously presented) A plant Plant comprising a cell according to claim 61.

66. (Currently amended) The plant Plant according to claim 65, wherein the plant is selected from the group comprising consisting of food plants, ornamental plants and medicinal plants and is preferably selected from the group comprising rice, maize, potatoes, tomatoes, rape, soya and sugar beet.

67. (Previously presented) The plant Plant according to claim 65, wherein the plant is a male, sterile plant and has at least one further modification of its genotype, particularly a wherein said modification is caused by genetic engineering.

68. (Currently amended) A seed Seed of a the plant according to claim 65, wherein said seed comprises said isolated nucleic acid sequence.

69. (Currently amended) An hybrid Hybrid seed, obtainable in that derived from crossing a the male, sterile plant according to claim 67 is hybridized with another male, fertile plant and, wherein the hybrid seed is obtained from the resulting filial generation of said crossing, and wherein said seed comprises said isolated nucleic acid sequence.

70. (Withdrawn) Process for the production of male, sterile plants, wherein a nucleic acid construct according to claim 55 is introduced into a cell, particularly into a plant cell and a plant is produced from said cell.

71. (Withdrawn) Process according to claim 70, wherein the plant is selected from the group comprising food plants, ornamental plants and medicinal plants and is preferably selected from the group comprising rice, maize, potatoes, tomatoes, rape, soya and sugar beet.

72. (Withdrawn) Use of a nucleic acid construct according to claim 55, for producing sterile, male plants.

73. (Currently amended) A method for expression of a nucleic acid sequence, wherein said method involving comprises using a nucleic acid sequence coding comprising for a both a tapetum-specific and a pollen-specific promoter, the and wherein said nucleic acid sequence comprising comprises a range of at least 900 contiguous nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1.

74. (Withdrawn) Restorer plant, characterized in that in one or more of its cells it comprises a nucleic acid coding for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising a range of at least 900 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1 as promoter and a nucleic acid coding for a further invertase, which is controlled by said promoter, the further invertase differing from the cell's own invertase.

75. (Withdrawn) Restorer plant, wherein in one or more of its cells it comprises a nucleic acid coding for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising a range of at least 900 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1 as promoter and a nucleic acid coding for a saccharose transport system and which is controlled by said promoter.

76. (Withdrawn) Restorer plant according to claim 75, wherein in one or more of its cells, it comprises a nucleic acid coding for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising a range of at least 900 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1 as promoter and a nucleic acid coding for saccharose synthase and/or cytoplasmically expressed invertase and whose expression is controlled by the promoter.

77. (Withdrawn) Plant, wherein in one or more of its cells, it comprises a nucleic acid construct according to claim 55 and the cell or cells further comprise a nucleic acid sequence coding

for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising a range of at least 900 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1 as promoter and a nucleic acid coding for a further invertase and which is controlled by said promoter, the further invertase differing from the cell's own invertase.

78. (Withdrawn) Plant, wherein in one or more of its cells, it comprises a nucleic acid construct according to claim 55 and the cell or cells also comprise a nucleic acid sequence coding for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising a range of at least 900 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1 as promoter and a nucleic acid coding for a saccharose transport system, which is controlled by said promoter.

79. (Withdrawn) Plant, according to claim 78, wherein in one or more of its cells, it comprises a nucleic acid construct according to claim 78 and the cell or cells also comprise a nucleic acid sequence coding for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising a range of at least 900 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1 as promoter and a nucleic acid coding for saccharose synthase and/or cytoplasmically expressed invertase, whose expression is controlled by the promoter.

80. (Withdrawn) Plant according to claim 74, wherein the further invertase, differing from the cell's own invertase, is

selected from the group of invertases comprising invertases of *Saccharomyces cerevisiae* and invertases of *Zymomonas mobilis*.

81. (Withdrawn) Plant according to claim 76, wherein the saccharose synthase is of a heterologous or homologous origin.

82. (Withdrawn) Plant according to claim 79, wherein the cytoplasmically expressed invertase is of a homologous or heterologous origin.

83. (Withdrawn) Plant according to claim 82, wherein the cytoplasmically expressed invertase is of a heterologous origin and is preferably selected from the group of invertases comprising invertases of *Saccharomyces cerevisiae* and invertases of *Zymomonas mobilis*.

84. (Withdrawn) Seed of a plant according to claim 74.

85. (Withdrawn) A method for in vitro embryogenesis of haploid or diploid or double diploid plants, comprising germinating a seed of claim 84.

86. (previously presented) ~~Fruit, particularly A~~ seedless fruit, of a plant according to claim 65.

87. (Withdrawn) Fruit of a plant according to claim 74.

88. (Withdrawn) Process for cloning promoters, which are functionally homologous to one of the promoters coding for a both tapetum-specific and pollen-specific promoter, the nucleic

acid sequence comprising a range of at least 900 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1, characterized by the following steps:

- c) cloning anther-specific invertase cDNA by RT-PCR of mRNA from anthers, including optionally using oligonucleotides OIN3 and OIN4,
- d) cloning the corresponding promoters.

89. (New) Plant according to claim 65, wherein the plant is selected from the group consisting of rice, maize, potatoes, tomatoes, rape, soya and sugar beet.